

1633  
#32165  
1600  
12/31/01

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/042,488B

DATE: 12/11/2001  
TIME: 10:26:16

Input Set : A:\SA1520-2.APP.txt  
Output Set: N:\CRF3\12112001\I042488B.raw

p.5

3 <110> APPLICANT: EVANS, RONALD M.  
 4 NO, DAVID  
 5 SAEZ, ENRIQUE  
 7 <120> TITLE OF INVENTION: METHODS FOR MODULATING EXPRESSION OF EXOGENOUS GENES IN  
 8 MAMMALIAN SYSTEMS, AND PRODUCTS RELATED THERETO  
 10 <130> FILE REFERENCE: SALK1520-2  
 12 <140> CURRENT APPLICATION NUMBER: 09/042,488B  
 13 <141> CURRENT FILING DATE: 1998-03-16  
 15 <150> PRIOR APPLICATION NUMBER: 08/974,530  
 16 <151> PRIOR FILING DATE: 1997-11-19  
 18 <150> PRIOR APPLICATION NUMBER: 08/628,830  
 19 <151> PRIOR FILING DATE: 1996-04-05  
 21 <160> NUMBER OF SEQ ID NOS: 18  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 71  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus  
 32 peptide sequence  
 34 <220> FEATURE:  
 35 <221> NAME/KEY: MOD\_RES  
 36 <222> LOCATION: (2)..(3)  
 37 <223> OTHER INFORMATION: Any amino acid  
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 40 <221> NAME/KEY: MOD\_RES  
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 45 <221> NAME/KEY: MOD\_RES /  
 46 <222> LOCATION: (8)  
 47 <223> OTHER INFORMATION: Any amino acid  
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 52 <223> OTHER INFORMATION: Any amino acid  
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 61 <222> LOCATION: (14)..(17)  
 62 <223> OTHER INFORMATION: Any amino acid  
 64 <220> FEATURE:  
 65 <221> NAME/KEY: MOD\_RES

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 71 <222> LOCATION: (23)  
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 76 <222> LOCATION: (26)  
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 117 <223> OTHER INFORMATION: Any amino acid  
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 121 1 5 10 15  
 W--> 123 Xaa Cys Xaa Xaa Cys Lys Xaa Phe Phe Xaa Arg Xaa Xaa Xaa Xaa Xaa  
 124 20 25 30  
 W--> 126 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys  
 127 35 40 45

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W1-> 129 Xaa Xaa Xaa Lys Xaa Xaa Arg Xaa Xaa Cys Xaa Xaa Cys Arg Xaa Xaa  
130 50 55 60  
W-> 132 Lys Cys Xaa Xaa Xaa Gly Met  
133 65 70  
136 <210> SEQ ID NO: 2  
137 <211> LENGTH: 5  
138 <212> TYPE: PRT  
139 <213> ORGANISM: Artificial Sequence  
141 <220> FEATURE:  
142 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
peptide  
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147 1 5  
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151 <211> LENGTH: 5  
152 <212> TYPE: PRT  
153 <213> ORGANISM: Artificial Sequence  
155 <220> FEATURE:  
156 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
peptide  
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161 1 5  
164 <210> SEQ ID NO: 4  
165 <211> LENGTH: 2241  
166 <212> TYPE: DNA  
167 <213> ORGANISM: Artificial Sequence  
169 <220> FEATURE:  
170 <223> OTHER INFORMATION: Description of Artificial Sequence: Recombinant  
VgEcR  
173 <220> FEATURE:  
174 <221> NAME/KEY: CDS  
175 <222> LOCATION: (1)..(2238)  
177 <400> SEQUENCE: 4  
178 atg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac 48  
179 Met Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp  
180 1 5 10 15  
182 ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat 96  
183 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp  
184 20 25 30  
186 ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 144  
187 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro  
188 35 40 45  
190 cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 192  
191 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe  
192 50 55 60  
194 gag cag atg ttt acc gat gcc ctt gga att gac gag tac ggt ggg aag 240  
195 Glu Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly Lys

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Input Set : A:\SA1520-2.APP.txt  
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196	65	70	75	80	
198	ctt cta ggt acc tct aga agg ata tcg aat tct ata tct tca ggt cgc				288
199	Leu Leu Gly Thr Ser Arg Arg Ile Ser Asn Ser Ile Ser Ser Gly Arg				
200	85	90	95		
202	gat gat ctc tcg cct tcg agc agc ttg aac gga tac tcg gcg aac gaa				336
203	Asp Asp Leu Ser Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asn Glu				
204	100	105	110		
206	agc tgc gat gcg aag aag agc aag aag gga cct gcg cca cgg gtg caa				384
207	Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala Pro Arg Val Gln				
208	115	120	125		
210	gag gag ctg tgc ctg gtt tgc ggc gac agg gcc tcc ggc tac cac tac				432
211	Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr				
212	130	135	140		
214	aac gcc ctc acc tgt gga tcc tgc aag gtg ttc ttt cga cgc agc gtt				480
215	Asn Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Arg Arg Ser Val				
216	145	150	155	160	
218	acg aag agc gcc tac tgc tgc aag ttc ggg cgc gcc tgc gaa atg				528
219	Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg Ala Cys Glu Met				
220	165	170	175		
222	gac atg tac atg agg cga aag tgt cag gag tgc cgc ctg aaa aag tgc				576
223	Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys				
224	180	185	190		
226	ctg gcc gtc ggt atg cgg ccg gaa tgc gtc gtc ccg gag aac caa tgt				624
227	Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys				
228	195	200	205		
230	gcg atg aag cgg cgc gaa aag aag gcc cag aag gag aag gac aaa atg				672
231	Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met				
232	210	215	220		
234	acc act tcg ccg agc tct cag cat ggc ggc aat ggc agc ttg gcc tct				720
235	Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser				
236	225	230	235	240	
238	ggt ggc gca gac ttt gtt aag aag gag att ctt gac ctt atg aca				768
239	Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr				
240	245	250	255		
242	tgc gag ccg ccc cag cat gcc act att ccg cta cta cct gat gaa ata				816
243	Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile				
244	260	265	270		
246	ttg gcc aag tgtcaa gcg cgc aat ata cct tcc tta acg tac aat cag				864
247	Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln				
248	275	280	285		
250	ttg gcc gtt ata tac aag tta att tgg tac cag gat ggc tat gag cag				912
251	Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln				
252	290	295	300		
254	cca tct gaa gag gat ctc agg cgt ata atg agt caa ccc gat gag aac				960
255	Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn				
256	305	310	315	320	
258	gag agc caa acg gac gtc agc ttt cgg cat ata acc gag ata acc ata				1008
259	Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile				
260	325	330	335		

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262	ctc acg gtc cag ttg att gtt gag ttt gct aaa ggt cta cca gcg ttt	1056
263	Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe	
264	340 345 350	
266	aca aag ata ccc cag gag gac cag atc acg tta cta aag gcc tgc tcg	1104
267	Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser	
268	355 360 365	
270	tcg gag gtg atg atg ctg cgt atg gca cga cgc tat gac cac agc tcg	1152
271	Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser	
272	370 375 380	
274	gac tca ata ttc ttc gcg aat aat aga tca tat acg cgg gat tct tac	1200
275	Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr	
276	385 390 395 400	
278	aaa atg gcc gga atg gct gat aac att gaa gac ctg ctg cat ttc tgc	1248
279	Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys	
280	405 410 415	
282	cgc caa atg ttc tcg atg aag gtg gac aac gtc gaa tac gcg ctt ctc	1296
283	Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu	
284	420 425 430	
286	act gcc att gtg atc ttc tcg gac cgg ccg ggc ctg gag aag gcc caa	1344
287	Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln	
288	435 440 445	
290	cta gtc gaa gcg atc cag agc tac tac atc gac acg cta cgc att tat	1392
291	Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr	
292	450 455 460	
294	ata ctc aac cgc cac tgc ggc gac tca atg agc ctc gtc ttc tac gca	1440
295	Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala	
296	465 470 475 480	
298	aag ctg ctc tcg atc ctc acc gag ctg cgt acg ctg ggc aac cag aac	1488
299	Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn	
300	485 490 495	
302	gcc gag atg tgt ttc tca cta aag ctc aaa aac cgc aaa ctg ccc aag	1536
303	Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys	
304	500 505 510	
306	ttc ctc gag gag atc tgg gac gtt cat gcc atc ccg cca tcg gtc cag	1584
307	Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro Ser Val Gln	
308	515 520 525	
310	tcg cac ctt cag att acc cag gag gag aac gag cgt ctc gag cgg gct	1632
311	Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu Glu Arg Ala	
312	530 535 540	
314	gag cgt atg cgg gca tcg gtt ggg ggc gcc att acc gcc ggc att gat	1680
315	Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala Gly Ile Asp	
316	545 550 555 560	
318	tgc gac tct gcc tcc act tcg gcg gca gcc gcg gcc cag cat cag	1728
319	Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Gln His Gln	
320	565 570 575	
322	cct cag cct cag ccc cag ccc caa ccc tcc tcc ctg acc cag aac gat	1776
323	Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr Gln Asn Asp	
324	580 585 590	
326	tcc cag cac cag aca cag ccg cag cta caa cct cag cta cca cct cag	1824

Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**  
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L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:1417 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:1465 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13